

SEQUENCE LISTING

<110> Suntory Limited

<120> MARCHANTIALES-DERIVED UNSATURATED FATTY ACID SYNTHETASE GENES

AND USE OF THE SAME

<130>

<150> JP 2003-425673

<151> 2003-12-22

<160> 46

<170> PatentIn Ver. 2.1

<210> 1

<211> 2519

<212> DNA

<213> Marchantia polymorpha

<220>

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<222> (253)..(1698)

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gtcggactga tcaactcagtc cgtcactgca aacgcgagcg agcgagagtg cgagtgagcg 180

agcgagcgag cgagagccgc ggtgtgtctg tgagatccaa tccttttct gctttgcgcg 240

ctgtggggcg cg atg gcc tcg tcc acc acc acc gcc gtg aag caa tct tcg 291

Met Ala Ser Ser Thr Thr Thr Ala Val Lys Gln Ser Ser

1 5 10

ggt ggg ctg tgg tcg aaa tgg ggc acc ggc agc aac ttg agc ttc gtg 339

Gly Gly Leu Trp Ser Lys Trp Gly Thr Gly Ser Asn Leu Ser Phe Val

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tcg cgc aag gag cag cag cag cag cag cag agc tct ccc gag gcg 387

Ser Arg Lys Glu Gln Gln Gln Gln Gln Gln Ser Ser Pro Glu Ala

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tcg act ccc gcg gcg cag cag gag aaa tcc atc agt aga gaa tcc atc 435

Ser Thr Pro Ala Ala Gln Gln Glu Lys Ser Ile Ser Arg Glu Ser Ile

50 55 60

Asn Val His His Ala Ala Thr Asn Glu Cys Asp Asp Lys Tyr Gln Pro
 255 260 265

atc gat ccc gac atc gac acc gtg ccc ctg ctc gcc tgg agc aag gaa 1107
 Ile Asp Pro Asp Ile Asp Thr Val Pro Leu Leu Ala Trp Ser Lys Glu
 270 275 280 285

atc ttg gcc acc gtc gac gac caa ttc ttc cga tcg atc atc agc gtg 1155
 Ile Leu Ala Thr Val Asp Asp Gln Phe Phe Arg Ser Ile Ile Ser Val
 290 295 300

cag cac ctt ctg ttc ttc ccg ctc ctc ttc ttg gca aga ttc agc tgg 1203
 Gln His Leu Leu Phe Phe Pro Leu Leu Phe Leu Ala Arg Phe Ser Trp
 305 310 315

ctg cat tcg agt tgg gcc cac gcc agc aac ttc gag atg cct cgg tac 1251
 Leu His Ser Ser Trp Ala His Ala Ser Asn Phe Glu Met Pro Arg Tyr
 320 325 330

atg aga tgg gcg gag aag gcc tcg ctc ctc ggg cac tac ggc gcc tca 1299
 Met Arg Trp Ala Glu Lys Ala Ser Leu Leu Gly His Tyr Gly Ala Ser
 335 340 345

atc ggc gcc gcc ttc tac att ttg ccc atc ccc cag gcc atc tgc tgg 1347
 Ile Gly Ala Ala Phe Tyr Ile Leu Pro Ile Pro Gln Ala Ile Cys Trp
 350 355 360 365

ctc ttc ttg tcg caa ctg ttt tgc ggc gct ctg ctc agc att gtc ttc 1395
 Leu Phe Leu Ser Gln Leu Phe Cys Gly Ala Leu Leu Ser Ile Val Phe
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 Val Ile Ser His Asn Gly Met Asp Val Tyr Asn Asp Pro Arg Asp Phe
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 Val Thr Ala Gln Val Thr Ser Thr Arg Asn Ile Glu Gly Asn Phe Phe
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aac gac tgg ttc acc gga ggc ctg aac agg cag att gag cac cat ctg 1539
 Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu
 415 420 425

ttt ccg tct ctt ccg agg cac aac ctc gcc aag gtc gcg cca cac gtc 1587
 Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Val Ala Pro His Val
 430 435 440 445

aag gcg ctc tgc gcc aag cac ggt ttg cat tac gaa gaa ttg agt ctg 1635
 Lys Ala Leu Cys Ala Lys His Gly Leu His Tyr Glu Glu Leu Ser Leu
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ggc acg gga gtc tgt cgt gtc ttc aat cgg cta gta gag gta gca tac 1683
 Gly Thr Gly Val Cys Arg Val Phe Asn Arg Leu Val Glu Val Ala Tyr
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gct gcg aaa gta tag atcgacgaga gttcccacc aacacagtta gaacaaggga 1738
 Ala Ala Lys Val
 480

atagtagcag agaaggagac agcaacctgg actttttgtt cctgatgttg catactttct 1798

cgaatatacg tctccacgcc ttcaagtttc agcttcaact gattgtcttc agtaaccatc 1858

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gcggtgaata gtaaagccaa ttcaacacat acgggagaag atgggtcgat attgtattt 2398

ggcaggggtg ccagatttca cccatcagtc tctcacttgc ttgtatgtcc ctgacgtgct 2458

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a 2519

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<211> 481

<212> PRT

<213> Marchantia polymorpha

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35 40 45

Ala Ala Gln Gln Glu Lys Ser Ile Ser Arg Glu Ser Ile Pro Glu Gly
 50 55 60
 Phe Leu Thr Val Glu Glu Val Ser Lys His Asp Asn Pro Ser Asp Cys
 65 70 75 80
 Trp Ile Val Ile Asn Asp Lys Val Tyr Asp Val Ser Ala Phe Gly Lys
 85 90 95
 Thr His Pro Gly Gly Pro Val Ile Phe Thr Gln Ala Gly Arg Asp Ala
 100 105 110
 Thr Asp Ser Phe Lys Val Phe His Ser Ala Lys Ala Trp Gln Phe Leu
 115 120 125
 Gln Asp Leu Tyr Ile Gly Asp Leu Tyr Asn Ala Glu Pro Val Ser Glu
 130 135 140
 Leu Val Lys Asp Tyr Arg Asp Leu Arg Thr Ala Phe Met Arg Ser Gln
 145 150 155 160
 Leu Phe Lys Ser Ser Lys Met Tyr Tyr Val Thr Lys Cys Val Thr Asn
 165 170 175
 Phe Ala Ile Leu Ala Ala Ser Leu Ala Val Ile Ala Trp Ser Gln Thr
 180 185 190
 Tyr Leu Ala Val Leu Cys Ser Ser Phe Leu Leu Ala Leu Phe Trp Gln
 195 200 205
 Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val Thr Glu
 210 215 220
 Asn Arg Ser Leu Asn Thr Tyr Phe Gly Gly Leu Phe Trp Gly Asn Phe
 225 230 235 240
 Ala Gln Gly Tyr Ser Val Gly Trp Trp Lys Thr Lys His Asn Val His
 245 250 255
 His Ala Ala Thr Asn Glu Cys Asp Asp Lys Tyr Gln Pro Ile Asp Pro
 260 265 270
 Asp Ile Asp Thr Val Pro Leu Leu Ala Trp Ser Lys Glu Ile Leu Ala
 275 280 285
 Thr Val Asp Asp Gln Phe Phe Arg Ser Ile Ile Ser Val Gln His Leu
 290 295 300
 Leu Phe Phe Pro Leu Leu Phe Leu Ala Arg Phe Ser Trp Leu His Ser
 305 310 315 320
 Ser Trp Ala His Ala Ser Asn Phe Glu Met Pro Arg Tyr Met Arg Trp
 325 330 335
 Ala Glu Lys Ala Ser Leu Leu Gly His Tyr Gly Ala Ser Ile Gly Ala
 340 345 350
 Ala Phe Tyr Ile Leu Pro Ile Pro Gln Ala Ile Cys Trp Leu Phe Leu
 355 360 365
 Ser Gln Leu Phe Cys Gly Ala Leu Leu Ser Ile Val Phe Val Ile Ser
 370 375 380
 His Asn Gly Met Asp Val Tyr Asn Asp Pro Arg Asp Phe Val Thr Ala
 385 390 395 400
 Gln Val Thr Ser Thr Arg Asn Ile Glu Gly Asn Phe Phe Asn Asp Trp
 405 410 415
 Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro Ser
 420 425 430
 Leu Pro Arg His Asn Leu Ala Lys Val Ala Pro His Val Lys Ala Leu
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Cys Ala Lys His Gly Leu His Tyr Glu Glu Leu Ser Leu Gly Thr Gly
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 <222> (194)..(1066)

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 cgaatccgcc gagagtcgat cgggattggg tagaaggagg agaaggagga gaagaggagg 180
 aggaggagca gcg atg gag gcg tac gag atg gtg gat agt ttt gtg tcg 229
 Met Glu Ala Tyr Glu Met Val Asp Ser Phe Val Ser
 1 5 10
 aag acg gtt ttc gaa acg ctg cag aga ctg agg ggc gga gtc gtg ttg 277
 Lys Thr Val Phe Glu Thr Leu Gln Arg Leu Arg Gly Gly Val Val Leu
 15 20 25
 acg gaa tct gcg atc acc aaa ggt ttg cca tgc gtc gat agc ccg acg 325
 Thr Glu Ser Ala Ile Thr Lys Gly Leu Pro Cys Val Asp Ser Pro Thr
 30 35 40
 ccg atc gtt ctt ggg ttg tcg tcc tac ttg aca ttc gtg ttt ctc ggg 373
 Pro Ile Val Leu Gly Leu Ser Ser Tyr Leu Thr Phe Val Phe Leu Gly
 45 50 55 60
 ctc att gtc atc aag agc ctg gat ctt aag ccc cgc tcc aag gag ccc 421
 Leu Ile Val Ile Lys Ser Leu Asp Leu Lys Pro Arg Ser Lys Glu Pro
 65 70 75
 gcc att ttg aac ctg ttt gtg atc ttc cac aac ttc gtc tgc ttc gca 469
 Ala Ile Leu Asn Leu Phe Val Ile Phe His Asn Phe Val Cys Phe Ala
 80 85 90
 ctc agt ctg tac atg tgc gtg gga att gtc cgt caa gct atc ctc aac 517
 Leu Ser Leu Tyr Met Cys Val Gly Ile Val Arg Gln Ala Ile Leu Asn

95	100	105	
agg tac tct ctg tgg ggc aat gcg tac aat ccc aaa gaa gtt caa atg 565			
Arg Tyr Ser Leu Trp Gly Asn Ala Tyr Asn Pro Lys Glu Val Gln Met			
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ggc cac ctg ctc tac att ttc tac atg tca aag tac atc gag ttt atg 613			
Gly His Leu Leu Tyr Ile Phe Tyr Met Ser Lys Tyr Ile Glu Phe Met			
125	130	135	140
gac acg gtc att atg att ttg aag cgc aac acg cgc cag atc act gtg 661			
Asp Thr Val Ile Met Ile Leu Lys Arg Asn Thr Arg Gln Ile Thr Val			
145	150	155	
ttg cat gtg tac cac cac gca tcc atc tcc ttc atc tgg tgg atc atc 709			
Leu His Val Tyr His His Ala Ser Ile Ser Phe Ile Trp Trp Ile Ile			
160	165	170	
gcc tac cat gct cct ggc ggt gaa gct tat ttc tct gcc gca ttg aac 757			
Ala Tyr His Ala Pro Gly Gly Glu Ala Tyr Phe Ser Ala Ala Leu Asn			
175	180	185	
tcc gga gta cat gtg ctc atg tac ctc tac tac ctt ttg gca gca act 805			
Ser Gly Val His Val Leu Met Tyr Leu Tyr Tyr Leu Leu Ala Ala Thr			
190	195	200	
ctg gga aag aac gag aaa gct cgc cgc aag tac cta tgg tgg gga aaa 853			
Leu Gly Lys Asn Glu Lys Ala Arg Arg Lys Tyr Leu Trp Trp Gly Lys			
205	210	215	220
tac ttg aca cag ctg cag atg ttc cag ttt gtc ctt aac atg att cag 901			
Tyr Leu Thr Gln Leu Gln Met Phe Gln Phe Val Leu Asn Met Ile Gln			
225	230	235	
gct tac tac gat att aag aac aac tcg cct tac cca caa ttt ttg atc 949			
Ala Tyr Tyr Asp Ile Lys Asn Asn Ser Pro Tyr Pro Gln Phe Leu Ile			
240	245	250	
cag att ttg ttc tac tac atg atc tcg ctt tta gcg cta ttt gga aac 997			
Gln Ile Leu Phe Tyr Tyr Met Ile Ser Leu Leu Ala Leu Phe Gly Asn			
255	260	265	
ttt tac gtt cac aaa tac gta tca gcg ccc gca aaa cct gcg aag atc 1045			
Phe Tyr Val His Lys Tyr Val Ser Ala Pro Ala Lys Pro Ala Lys Ile			
270	275	280	
aag agc aaa aag gca gaa taa gacaccaccc tagtgacaag aagattttac 1096			
Lys Ser Lys Lys Ala Glu			
285	290		

actaaactgt agtttagca cccatcggtg acacgaatac attctgggtc tgcctgtctt 1156
 ggaagagtcg aagcattcag gagctctccc gttccatcga tcaaactcgg aacgaagtgc 1216
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a 1577

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 <213> Marchantia polymorpha

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 35 40 45
 Gly Leu Ser Ser Tyr Leu Thr Phe Val Phe Leu Gly Leu Ile Val Ile
 50 55 60
 Lys Ser Leu Asp Leu Lys Pro Arg Ser Lys Glu Pro Ala Ile Leu Asn
 65 70 75 80
 Leu Phe Val Ile Phe His Asn Phe Val Cys Phe Ala Leu Ser Leu Tyr
 85 90 95
 Met Cys Val Gly Ile Val Arg Gln Ala Ile Leu Asn Arg Tyr Ser Leu
 100 105 110
 Trp Gly Asn Ala Tyr Asn Pro Lys Glu Val Gln Met Gly His Leu Leu
 115 120 125
 Tyr Ile Phe Tyr Met Ser Lys Tyr Ile Glu Phe Met Asp Thr Val Ile
 130 135 140
 Met Ile Leu Lys Arg Asn Thr Arg Gln Ile Thr Val Leu His Val Tyr
 145 150 155 160
 His His Ala Ser Ile Ser Phe Ile Trp Trp Ile Ile Ala Tyr His Ala
 165 170 175
 Pro Gly Gly Glu Ala Tyr Phe Ser Ala Ala Leu Asn Ser Gly Val His
 180 185 190
 Val Leu Met Tyr Leu Tyr Tyr Leu Leu Ala Ala Thr Leu Gly Lys Asn

195	200	205	
Glu Lys Ala Arg Arg Lys Tyr Leu Trp Trp Gly Lys Tyr Leu Thr Gln			
210	215	220	
Leu Gln Met Phe Gln Phe Val Leu Asn Met Ile Gln Ala Tyr Tyr Asp			
225	230	235	240
Ile Lys Asn Asn Ser Pro Tyr Pro Gln Phe Leu Ile Gln Ile Leu Phe			
245	250	255	
Tyr Tyr Met Ile Ser Leu Leu Ala Leu Phe Gly Asn Phe Tyr Val His			
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Lys Tyr Val Ser Ala Pro Ala Lys Pro Ala Lys Ile Lys Ser Lys Lys			
275	280	285	
Ala Glu			
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<220>
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 <222> (375)..(1829)

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 gctggacgta cagccggtgc tggaaattga tttgtgaaa agcgagccta cctctatcca 300
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 gaaggtcgac agtt atg ccg cca cac gcc cct gac tcc aca ggt ctt ggg 410
 Met Pro Pro His Ala Pro Asp Ser Thr Gly Leu Gly
 1 5 10
 ccc gaa gtt ttc cgc ctg cct gat gac gcg atc ccg gcc cag gat cgc 458
 Pro Glu Val Phe Arg Leu Pro Asp Ala Ile Pro Ala Gln Asp Arg
 15 20 25
 aga tct aca cag aag aaa tac tcg ctt tca gac gtc agc aag cac aac 506
 Arg Ser Thr Gln Lys Lys Tyr Ser Leu Ser Asp Val Ser Lys His Asn
 30 35 40

act ccg aat gat tgc tgg ctc gta att tgg ggg aag gtg tac gat gtt 554
 Thr Pro Asn Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val
 45 50 55 60

act tcg tgg gtt aag gtc cat cca ggt gga agt ctc atc ttt gtg aag 602
 Thr Ser Trp Val Lys Val His Pro Gly Gly Ser Leu Ile Phe Val Lys
 65 70 75

gcg gga cag gat tca aca caa ctc ttt gat tct tat cac ccc ctc tat 650
 Ala Gly Gln Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr
 80 85 90

gtc aga aag cta ctt gca cag ttc tgc att ggt gaa ctc caa acg agt 698
 Val Arg Lys Leu Leu Ala Gln Phe Cys Ile Gly Glu Leu Gln Thr Ser
 95 100 105

gcg gga gat gag aag ttc aag tct tca acg ttg gag tat gct ggt gaa 746
 Ala Gly Asp Glu Lys Phe Lys Ser Ser Thr Leu Glu Tyr Ala Gly Glu
 110 115 120

gaa cat gaa gta ttt tac cac act ctc aag cag cgc gtg gaa acg tac 794
 Glu His Glu Val Phe Tyr His Thr Leu Lys Gln Arg Val Glu Thr Tyr
 125 130 135 140

ttc cgc aag cag aag ata aat cct cga tac cat ccg caa atg ctt gtg 842
 Phe Arg Lys Gln Lys Ile Asn Pro Arg Tyr His Pro Gln Met Leu Val
 145 150 155

aag tca gcc gtg atc att gga acc ctt ctt ctc tgt tac tat ttt ggc 890
 Lys Ser Ala Val Ile Ile Gly Thr Leu Leu Leu Cys Tyr Tyr Phe Gly
 160 165 170

ttc ttc tgg tct caa aat gta ctc ctc tcg atg ttt ctg gca agc atc 938
 Phe Phe Trp Ser Gln Asn Val Leu Leu Ser Met Phe Leu Ala Ser Ile
 175 180 185

atg ggg ttc tgc act gcg gag gtg ggc atg tcc atc atg cac gat ggt 986
 Met Gly Phe Cys Thr Ala Glu Val Gly Met Ser Ile Met His Asp Gly
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 Asn His Gly Ser Tyr Thr Gln Ser Thr Leu Leu Gly Tyr Val Met Gly
 205 210 215 220

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 Ala Thr Leu Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln
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cat gtg gcc ggg cac cac tcg ttc acc aac atc gac cat tac gat cca 1130
 His Val Ala Gly His His Ser Phe Thr Asn Ile Asp His Tyr Asp Pro

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Asp Ile Arg Val Lys Asp Pro Asp Leu Arg Arg Val Thr Ser Gln Gln			
255	260	265	
ccc cga aga tgg ttt cac gag tat cag cat atc tac tta gga gta ctc 1226			
Pro Arg Arg Trp Phe His Glu Tyr Gln His Ile Tyr Leu Gly Val Leu			
270	275	280	
tat ggc gtt ctt gcc tta aaa agt gtg ttg att gat gat ttc agc gcc 1274			
Tyr Gly Val Leu Ala Leu Lys Ser Val Leu Ile Asp Asp Phe Ser Ala			
285	290	295	300
ttc ttc agt ggt gct atc ggc cca gta aag ata gct caa atg aca cca 1322			
Phe Phe Ser Gly Ala Ile Gly Pro Val Lys Ile Ala Gln Met Thr Pro			
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320	325	330	
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335	340	345	
att ggt ctc tac att ctc tca cag tta gtt gca ggg tgg act ctt gcc 1466			
Ile Gly Leu Tyr Ile Leu Ser Gln Leu Val Ala Gly Trp Thr Leu Ala			
350	355	360	
ctc ttc ttt caa gta gca cac gtt gtc gac gat gca gta ttt ccc gtt 1514			
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Ala Glu Thr Asp Gly Gly Lys Ala Lys Ile Pro Ser Gly Trp Ala Glu			
385	390	395	
atg cag gtc aga acc act acc aat ttc agc tca cga tca atg ttc tgg 1610			
Met Gln Val Arg Thr Thr Thr Asn Phe Ser Ser Arg Ser Met Phe Trp			
400	405	410	
aca cat att agt ggc ggt ctg aac cat cag atc gag cac cat ctt ttc 1658			
Thr His Ile Ser Gly Gly Leu Asn His His Gln Ile Glu His His Leu Phe			
415	420	425	
ccg ggt gtc tgt cat gtt cac tac cca agc ata cag cca atc gtg aag 1706			
Pro Gly Val Cys His Val His Tyr Pro Ser Ile Gln Pro Ile Val Lys			
430	435	440	

gct acc tgt gac gag ttc aac gtg cct tat act tcc tac ccc act ttc 1754
 Ala Thr Cys Asp Glu Phe Asn Val Pro Tyr Thr Ser Tyr Pro Thr Phe
 445 450 455 460

tgg gcg gcc ctt agg gca cat ttt caa cat ctg aaa aac gtc gga cta 1802
 Trp Ala Ala Leu Arg Ala His Phe Gln His Leu Lys Asn Val Gly Leu
 465 470 475

caa gat gga cta cga ctg gat ggc tga actgtgacag catgctttgg 1849
 Gln Asp Gly Leu Arg Leu Asp Gly
 480 485

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<210> 6

<211> 484

<212> PRT

<213> Marchantia polymorpha

<400> 6

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 35 40 45
 Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp Val
 50 55 60
 Lys Val His Pro Gly Gly Ser Leu Ile Phe Val Lys Ala Gly Gln Asp
 65 70 75 80
 Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys Leu
 85 90 95
 Leu Ala Gln Phe Cys Ile Gly Glu Leu Gln Thr Ser Ala Gly Asp Glu
 100 105 110
 Lys Phe Lys Ser Ser Thr Leu Glu Tyr Ala Gly Glu Glu His Glu Val

(12)

115 120 125
 Phe Tyr His Thr Leu Lys Gln Arg Val Glu Thr Tyr Phe Arg Lys Gln
 130 135 140
 Lys Ile Asn Pro Arg Tyr His Pro Gln Met Leu Val Lys Ser Ala Val
 145 150 155 160
 Ile Ile Gly Thr Leu Leu Leu Cys Tyr Tyr Phe Gly Phe Phe Trp Ser
 165 170 175
 Gln Asn Val Leu Leu Ser Met Phe Leu Ala Ser Ile Met Gly Phe Cys
 180 185 190
 Thr Ala Glu Val Gly Met Ser Ile Met His Asp Gly Asn His Gly Ser
 195 200 205
 Tyr Thr Gln Ser Thr Leu Leu Gly Tyr Val Met Gly Ala Thr Leu Asp
 210 215 220
 Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln His Val Ala Gly
 225 230 235 240
 His His Ser Phe Thr Asn Ile Asp His Tyr Asp Pro Asp Ile Arg Val
 245 250 255
 Lys Asp Pro Asp Leu Arg Arg Val Thr Ser Gln Gln Pro Arg Arg Trp
 260 265 270
 Phe His Glu Tyr Gln His Ile Tyr Leu Gly Val Leu Tyr Gly Val Leu
 275 280 285
 Ala Leu Lys Ser Val Leu Ile Asp Asp Phe Ser Ala Phe Phe Ser Gly
 290 295 300
 Ala Ile Gly Pro Val Lys Ile Ala Gln Met Thr Pro Leu Glu Met Gly
 305 310 315 320
 Val Phe Trp Gly Gly Lys Val Val Tyr Ala Leu Tyr Met Phe Leu Leu
 325 330 335
 Pro Met Met Tyr Gly Gln Tyr Asn Ile Leu Thr Phe Ile Gly Leu Tyr
 340 345 350
 Ile Leu Ser Gln Leu Val Ala Gly Trp Thr Leu Ala Leu Phe Phe Gln
 355 360 365
 Val Ala His Val Val Asp Asp Ala Val Phe Pro Val Ala Glu Thr Asp
 370 375 380
 Gly Gly Lys Ala Lys Ile Pro Ser Gly Trp Ala Glu Met Gln Val Arg
 385 390 395 400
 Thr Thr Thr Asn Phe Ser Ser Arg Ser Met Phe Trp Thr His Ile Ser
 405 410 415
 Gly Gly Leu Asn His Gln Ile Glu His His Leu Phe Pro Gly Val Cys
 420 425 430
 His Val His Tyr Pro Ser Ile Gln Pro Ile Val Lys Ala Thr Cys Asp
 435 440 445
 Glu Phe Asn Val Pro Tyr Thr Ser Tyr Pro Thr Phe Trp Ala Ala Leu
 450 455 460
 Arg Ala His Phe Gln His Leu Lys Asn Val Gly Leu Gln Asp Gly Leu
 465 470 475 480
 Arg Leu Asp Gly

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tgggtggaarg anaarcayaa 20

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<223> i

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rttnarncn ccngtraacc a 21

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<210> 10

<211> 22

<212> DNA

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<210> 11

<211> 20

<212> DNA

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gtngarttya tggayacngt 20

<210> 12

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cknccccara anarrtaytt 20

<210> 13
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tatgatttg aagcgcaaca cg 22

<210> 15
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athrangrna artntaygay gt

22

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ggnaynkwnt sdatrtcngg rtc

23

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gtgtgtacga tccgtggta cc 22

<210> 18

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<400> 18
aaggcgggac aggattcaac ac 22

<210> 19

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<213> Artificial Sequence

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<210> 20

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<210> 22
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<210> 25
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<400> 25

cgggatcctc tctggcgca ccatcgtc 28

<210> 26

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<212> DNA

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<223> Description of Artificial Sequence:Primer

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ggggtaccaa cgcgtttcc caccaacg 28

<210> 27

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<400> 27

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<210> 28

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<400> 28

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<210> 29

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<400> 30
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<210> 31
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gctctagaga cagttatgcc gccacacgc 29

<210> 32
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<400> 32
gctctagaag gcccaaagca tgctgtcac 29

<210> 33
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<400> 33
caggaaacag ctatgacc 18
(21)

<210> 34
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<210> 35
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<400> 35
ccggaattcg catgcctgca ggtccccaga 30

<210> 36
<211> 18
<212> DNA
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<220>
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<400> 36
tgtaaacga cggccagt 18

<210> 37
<211> 7
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<220>
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<222> (4)
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acid sequence

<400> 37

Trp Trp Lys Xaa Lys His Asn
1 5

<210> 38

<211> 7

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:conserved amino
acid sequence

<400> 38

Trp Phe Thr Gly Gly Leu Asn
1 5

<210> 39

<211> 7

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:conserved amino
acid sequence

<400> 39

Val Glu Phe Met Asp Thr Val
1 5

<210> 40

<211> 7

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:conserved amino
acid sequence

<400> 40

Lys Tyr Leu Phe Trp Gly Arg
1 5

<210> 41

<211> 8

<212> PRT

<213> Unknown Organism

<220>
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acid sequence

<220>
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<222> (2)
<223> Glu or Asn

<220>
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<222> (3)
<223> Gly or Asp

<400> 41
Ile Xaa Xaa Lys Val Tyr Asp Val
1 5

<210> 42
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acid sequence

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<223> Gln or Asp

<220>
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<223> Tyr or Thr

<220>
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<223> Met or Val

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Asp Pro Asp Ile Xaa Xaa Xaa Pro
1 5

<210> 43

<211> 26
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XbaMpELOf

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agtctctaga gcgatggagg cgtacg 26

<210> 44
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<212> DNA
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SacMpELOr

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cagtgagctc ggtgtcttat tctgcc 26

<210> 45
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<400> 45
agcttctaga gccatgccgc cacacgcc 29

<210> 46
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<212> DNA
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<220>
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<400> 46
cagtgagctc tcagccatcc agtcgt 26